

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2003, 21:58:12 ; Search time 24 Seconds
(without alignments)
719.636 Million cell updates/sec

Title: US-09-815-923-4

Sequence: 1 MPPSDAPPAPAPPPDLPAT.....TIOREVTISPPADSLCNL 587

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents-AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1726	55.0	630	US-07-959-943-11	Sequence 11, App1
2	1712	54.5	630	US-07-959-943-9	Sequence 9, App1
3	1710	54.4	607	US-07-959-943-7	Sequence 7, App1
4	1699	54.1	607	US-07-879-617A-12	Sequence 12, App1
5	1699	54.1	607	US-08-753-985-12	Sequence 12, App1
6	1664.5	53.0	653	US-07-782-298-2	Sequence 2, App1
7	1605.5	51.1	617	US-07-879-617A-11	Sequence 11, App1
8	1605.5	51.1	617	US-08-301-722A-3	Sequence 3, App1
9	1605.5	51.1	617	US-08-240-783B-3	Sequence 3, App1
10	1605.5	51.1	617	US-08-753-985-11	Sequence 11, App1
11	1605.5	51.1	617	US-09-084-813-3	Sequence 3, App1
12	1605.5	51.1	617	PCT-US92-09662-3	Sequence 3, App1
13	1542	49.1	620	US-08-301-722A-2	Sequence 2, App1
14	1525	48.6	619	US-07-762-132A-2	Sequence 2, App1
15	1525	48.6	619	US-08-301-722A-4	Sequence 4, App1
16	1476.5	47.0	616	US-07-879-617A-13	Sequence 13, App1
17	1476.5	47.0	616	US-08-753-985-13	Sequence 13, App1
18	1369.5	43.6	797	US-09-182-728A-2	Sequence 2, App1
19	1369.5	43.6	797	US-09-795-232-2	Sequence 2, App1
20	1368.5	43.6	797	US-08-700-013B-19	Sequence 19, App1
21	1368.5	43.6	797	US-09-191-468-124	Sequence 124, App
22	1367.5	43.5	797	US-09-191-468-122	Sequence 122, App
23	1363.5	43.4	797	US-08-191-468-120	Sequence 120, App
24	1363.5	43.4	799	US-08-700-013B-27	Sequence 27, App1
25	1360.5	43.3	797	US-08-700-013B-21	Sequence 21, App1
26	1358.5	43.3	599	US-08-301-722A-5	Sequence 5, App1
27	1347.5	42.9	599	US-08-295-814E-11	Sequence 11, App1

28	1347.5	42.9	599	US-08-240-783B-4	Sequence 4, App1
29	1347.5	42.9	599	US-09-084-813-4	Sequence 4, App1
30	1347.5	42.9	599	US-09-343-361-11	Sequence 11, App1
31	1347.5	42.9	599	PCT-US82-09662-4	Sequence 4, App1
32	1322.5	42.1	599	US-07-879-617A-10	Sequence 10, App1
33	1322.5	42.1	599	US-08-753-985-10	Sequence 10, App1
34	1271	40.5	627	US-08-295-814E-4	Sequence 4, App1
35	1271	40.5	627	US-09-343-361-4	Sequence 4, App1
36	1271	40.5	627	PCT-US93-01959-4	Sequence 4, App1
37	1256.5	40.0	614	US-08-295-814E-12	Sequence 12, App1
38	1256.5	40.0	614	US-09-343-361-12	Sequence 12, App1
39	1255	40.0	627	US-08-291-299-10	Sequence 10, App1
40	1255	40.0	627	PCT-US95-10579-10	Sequence 10, App1
41	1254	39.9	602	US-08-295-814E-2	Sequence 2, App1
42	1254	39.9	602	US-09-343-361-2	Sequence 2, App1
43	1254	39.9	602	PCT-US83-01959-2	Sequence 2, App1
44	1253.5	39.9	614	US-08-291-299-8	Sequence 8, App1
45	1253.5	39.9	614	PCT-US95-10579-8	Sequence 8, App1

ALIGNMENTS

```
RESULT 1
US-07-959-943-11
; Sequence 11, Application US/07959943
; Patent No. 5418162
; GENERAL INFORMATION:
; APPLICANT: Blakely, Randy D.
; APPLICANT: Fremieu Jr., Robert T.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Serotonin Transporter CDNA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park
; ADDRESSEE: and
; ADDRESS: Gibson
; STREET: Post Office Drawer 31107
; CITY: Raleigh
; STATE: NO. 5418162ch Carolina
; COUNTRY: U.S.A.
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,943
; FILING DATE: 19921014
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405.38a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-943-11

Query Match          55.0%; Score 1726; DB 1; Length 630;
Best Local Similarity 54.5%; Pred. No. 1.3e-149;
Matches 320; Conservative 97; Mismatches 154; Indels 16; Gaps 6;

OY 6 APPAPAPPP---DIPATTAQKRSRVVSLTPARORETWAKKAFLLAAGVADLGNW 62
DB 49 AVPSPCAGDTRHSIPATP-----TTLVAELHOGREBTGWKKVDFLLSYIGVAVDGNW 103
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[illegible][illegible]

Db	148	YIASYNTITIAAMLYLSSL--TDRLPMSTCSMTNMGCTNYPAQDINTWTLHSTP	204
Qy	187	AKFEERNLEQHSKSGDDMGPIKPSALCYGVFVLVYTSLKGVRSACKVWWTALA	246
Db	205	AEEFYLRHVLQIHSKGLODGLTISWOLTCIVLLFTFYFYSIMKGVKTSKVWWTATP	264
Qy	247	PYVVLILLARGVLTGATEGIRYVLTPEMHLOMSKVIDAASQIFSPGPGFTLLAL	306
Db	265	PYIVSLVLYRGATLTFGANRGVVFLLPKRMOKLLETGYVWVAADQIFSLPGFVLLAF	324
Qy	307	SSYNKNNNCYRDALTTSSINCLTSELAGVFYSVLGYMAHVONKSIEEGL-CPGLV	365
Db	325	ASYNKNNNCYQDALVTSVNCMTSPVSQFVFTVLGYMAEMRNDSEVAKDQPSLFF	384
Qy	366	IVYPELAIMTGSVFVAIFLFLMLITLGLDSTFGGLEAVTTALCDEYPRVIGRHREYVA	425
Db	385	ITFAEAIAMNPASTFFAIFLFLMLITLGLDSTFGALCEVITAVLDEPFIHAKRREVF	444
Qy	426	VLLFLFYICALPTTGTGGVYLDLNVYGPGLILEYVFAEAGACWYGVDRSEVRT	485
Db	445	IVVITCVLSGLTLTSGGAYVVTLLLEBATGPAVLTVALIERVAWSWYGTGTOPCSYKE	504
Qy	486	MLGHTPGMFWRCMSYISVPFLVLVEFVSLAHEMLGEGEYTSWSTLVGVWVTGTVS	545
Db	505	MLGSPGMFWRCMVASIPFLFLFITCSPLMSPQLRLPQYNYPHMSIVLGTGIGMSVI	564
Qy	546	CIPLYITIKLITPGNCINR-IKTIQREPVYSIPAD	581
Db	565	CIPLYITIRLISTPGTLERIKRISTTPEPTEIIPGCD	601

RESULT 5
 US-08-753-985-12
 Sequence 12, Application US/08753985
 Patent No. 5759788
 GENERAL INFORMATION:
 APPLICANT: Fremeanu Jr., Robert T.
 APPLICANT: Caron, Marc G.
 APPLICANT: Blakely, Randy D.
 TITLE OF INVENTION: A High Affinity L-Proline Transporter
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kilpatrick & Cody
 STREET: 1100 Peachtree Street, Suite 2800
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30309
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,985
 FILING DATE: 03-DEC-1996
 CLASSIFICATION: 356
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/879617
 FILING DATE: 01-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: EMU109
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6508
 TELEFAX: 404-815-6555
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 607 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

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? MOLECULE TYPE: protein
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? ORGANISM: Rattus
? TISSUE TYPE: Brain - serotonin transporter
? FEATURE:
? NAME/KEY: Active-site
? LOCATION: 95..96
? OTHER INFORMATION: /note= "Leucine zipper motif"
? FEATURE:
? NAME/KEY: Active-site
? LOCATION: 102..103
? OTHER INFORMATION: /note= "Leucine zipper motif"
? FEATURE:
? NAME/KEY: Active-site
? LOCATION: 109..110
? OTHER INFORMATION: /note= "Leucine zipper motif"
? FEATURE:
? NAME/KEY: Active-site
? LOCATION: 116..117
? OTHER INFORMATION: /note= "Leucine zipper motif"
US-08-753-985-12

Query Match      54.1%   Score 1699; DB 1; Length 607;
Best Local Similarity    54.4%   Pred No. 3.8e-147;
Matches 314; Conservative 98; Mismatches 149; Indels 16; Gaps 6;

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Query Match      54.1% Score 1699: DB 1:      length 607:
Best Local Similarity 54.4% Pred. No. 3.8e-147:
Matches 314: Conservative 98: Mismatches 149: Indels 16: Gaps 6:

OY 18 PATAA -OKRSVSVLNP-----ARQRETMAKKAFFLAVVGFVADVLGNVREPYICY 69
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 28 PGTSAGDEASHSIPATTTTLLVAELIKQGERETIMGKKMDLLSYIGVAVDLGNIMRPPICY 87
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 70 QNGGGAFLIPPCWMLIFEGCLPLFLELALSGYHRGCGCLTLKRICPALKGYALCMIDI 129
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 88 QNGGGAFLPLPTIIMAFIFGIFPLFYMELALQGYHRGCGCISIMRKICPIKIGIGALCIAF 147
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 130 YMGMYNTIICMAYVILFASLASINSVLPMTSCDQENMTPLCTPTSPOT--NPNSSTP 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 148 YIASYNTIIMALTYLISL---TDRLPMISCTNSMWTGACTNFPADDNITWTLHSTSP 204
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 187 AKFEFFERNVLEOHKNSGLDDMGPIKPSALCVFEGVLYLVFSLMKGVRSACKVWVTALA 246
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 205 AEEFLRHVLDIOHSGKQDQDGTISMQTLTLCIVLIFVIYFVSIMKGVTSGKWVWTATMF 264
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 247 PYVVLILLAGVILPGATBEGIRYILTPEDMKHLQNSKWIIDAASQIFFSLSRGFETLLAL 306
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 265 PYIYLSVLLVGCATLFGAMRGVVEFLAKPMOKLLETGWVWAAAQIFFSLSRGFEVLLAF 324
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 307 SSYNFNKNNCRDALITSSINCLTSFLGAFIYFSLVGMAYHQQNSISEVGLE -GGGLVF 365
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 325 ASYNKFNKNNCQDALVTSVNMCMSTFVSGFIYFTLGTGMAEKRNDESEVAKDAGPSLTF 384
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 366 IYVPEALATMTGVSFWALIFFLMLITLGLDSTFGGLEAVTALCDQEPYRLVGRHREVEVA 425
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 385 ITVEALAINMPASTFEFFALIFFLMLITLGLDSTFAGLEGVITAVLDEDFPHIAKREMPVL 444
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 426 VLLFETIYICALPTTGYGVLYVDLLNLYGPGALIFVFAFADAGCWYYGADRPSEDPRT 485
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 445 IVTITCVIGSLTTLTSGAVVVTLLLEEVATGPAYITALIAVAVASWVGITQFCSVKE 504
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 486 MLGHTPGWFMRTCSYISPVFLVLFVYSVAHEEMLEGETEYTSMTITGVWMTGTVVS 545
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 505 MLGSPGFMWICWVAISPLFLFLFICGFSMLSPQLRLFOYNTPHMSIVLGTGICOMSSVI 564
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 546 CIPLYIIVKLLITPGNCINR-IKTIOREPVTSIPAD 581
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 565 CIPYIIVRLISTPGLTKERITIKSITPETPEIPICGD 601
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
US-07-782-298-2
Sequence 2, Application US/07782298

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Query Match 51.1%; Score 1605.5; DB 1; Length 617;
Best Local Similarity 51.6%; Pred. No. 1.4e-138;
Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;

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QY 1 MPSPDAPP---APPAAPPDLPAA-TTAAQ-----KSRSVVSLT-----PARQRETMAKKAEEF 47
DB 6 MNPOVQPPNNGADGPEQPEQLRARKRTAEELVVERKNGVOCCLAPRDGDAQPRETWGKKIDF 65
OY 48 LLAVGFAVDLGNVWRPFYICONGGAFILPYCVMLEFGSLPFLFELALAGVYRGCCL 107
DB 66 LLSVVGFAVDLANVWRPFYICONGGAFILPYLFLIAGPLFYMELAGQVNRREGAA 125
OY 108 TLMKRICPALKGVGAICMIDYMGMYNTIIGNAVYVLIASLASINSVLPWTSCDNEWN 167
DB 126 TWMK-ICPFKGVGAVAILALVGYFYVNIAMSLYLFSSP-TLN--LPWTDCGHTWN 181
OY 168 TPCLCT-----PYSPT--NPNSSTPAKEFEFERNVLEQKSKNGCLDMGPIKSLALCV 218
DB 182 SPNCTDPKLLNGSVLGNHTKYSKYKFTPPAAEFYERGVLLHSSGIDHIGLPOMQLLCL 241
OY 219 FGVEVLVYFSLMKGVRSAGKVVWVTALAPYVLLILLAGVTLPGATEGIRYVLTPEMHK 278
DB 242 MVVIVLVLFSLMKGVKTSKGKVVWITATLPYFVLVYLHVGYTLPGASGIAVYLIHIDFYR 301
OY 279 LQNSKWIDAASQIFSLGPGFGLLALSSYNKFNNNCYRDALITSSINCLTSFLAGFYI 338
DB 302 LKEATVWIDATQIFFSLAGFGLVLIASFYNKFDNNCYRDALITSSINCLTSFVSGFAI 361
OY 339 FSVLGMAHVONKSTEEVLEGEGPLVIFYPEALATMTGVSFMAIIFFLMILITGLDSTF 398
DB 362 FSLIGMAHEKVNIEDVATEGAGVLFILYPEAISTLSGSTFMAVVFVMLALGLDSSM 421
OY 399 GGLEAVTTALCDEYPRVLRHREVEVAVLLFIYICALPTTYGGVYVLDLNVYGPGLA 458
DB 422 GGMNAVITGLADD-QVLAKRHRKLFTEGVTSTELLALFCTIKGIYVLTLDFFAAGTS 480
OY 459 ILFVFAEAGVGVNVDRESEDEVRTMLGHTPGEMFMTCSYISPVLLVLFVSVLAH 518
DB 481 ILFVFAEAGVGVNVDRESEDEVRTMLGHTPGEMFMTCSYISPVLLVLFVSVLAH 540
OY 519 EEMLGGEITYPSWSTIYGVWMTGTVVSCIPLYITIKLLITPGNCINRIKTIQORE 573
DB 541 KPLTYDDYIFPPMANWGMGIALSSMVLPTVITYIKFLSTOGSLMERLAVGITPE 595
```

RESULT 8
US-08-301-722A-3
Sequence 3, Application US/08301722A
Patent No. 5756307
GENERAL INFORMATION:
APPLICANT: Uhl, George R.
APPLICANT: Vandenberg, David
APPLICANT: Persico, Antonio
TITLE OF INVENTION: SEQUENCE OF HUMAN DOPAMINE TRANSPORTER
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301.722A
FILING DATE: 07-SEP-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1173-406P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..617
OTHER INFORMATION: /note="Hnat sequence, see Fig. 5"

Query Match 51.1%; Score 1605.5; DB 1; Length 617;
Best Local Similarity 51.6%; Pred. No. 1.4e-138;
Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;

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QY 1 MPSPDAPP---APPAAPPDLPAA-TTAAQ-----KSRSVVSLT-----PARQRETMAKKAEEF 47
DB 6 MNPOVQPPNNGADGPEQPEQLRARKRTAEELVVERKNGVOCCLAPRDGDAQPRETWGKKIDF 65
OY 48 LLAVGFAVDLGNVWRPFYICONGGAFILPYCVMLEFGSLPFLFELALAGVYRGCCL 107
DB 66 LLSVVGFAVDLANVWRPFYICONGGAFILPYLFLIAGPLFYMELAGQVNRREGAA 125
OY 108 TLMKRICPALKGVGAICMIDYMGMYNTIIGNAVYVLIASLASINSVLPWTSCDNEWN 167
DB 126 TWMK-ICPFKGVGAVAILALVGYFYVNIAMSLYLFSSP-TLN--LPWTDCGHTWN 181
OY 168 TPCLCT-----PYSPT--NPNSSTPAKEFEFERNVLEQKSKNGCLDMGPIKSLALCV 218
DB 182 SPNCTDPKLLNGSVLGNHTKYSKYKFTPPAAEFYERGVLLHSSGIDHIGLPOMQLLCL 241
OY 219 FGVEVLVYFSLMKGVRSAGKVVWVTALAPYVLLILLAGVTLPGATEGIRYVLTPEMHK 278
DB 242 MVVIVLVLFSLMKGVKTSKGKVVWITATLPYFVLVYLHVGYTLPGASGIAVYLIHIDFYR 301
OY 279 LQNSKWIDAASQIFSLGPGFGLLALSSYNKFNNNCYRDALITSSINCLTSFLAGFYI 338
DB 302 LKEATVWIDATQIFFSLAGFGLVLIASFYNKFDNNCYRDALITSSINCLTSFVSGFAI 361
OY 339 FSVLGMAHVONKSTEEVLEGEGPLVIFYPEALATMTGVSFMAIIFFLMILITGLDSTF 398
DB 362 FSLIGMAHEKVNIEDVATEGAGVLFILYPEAISTLSGSTFMAVVFVMLALGLDSSM 421
OY 399 GGLEAVTTALCDEYPRVLRHREVEVAVLLFIYICALPTTYGGVYVLDLNVYGPGLA 458
DB 422 GGMNAVITGLADD-QVLAKRHRKLFTEGVTSTELLALFCTIKGIYVLTLDFFAAGTS 480
OY 459 ILFVFAEAGVGVNVDRESEDEVRTMLGHTPGEMFMTCSYISPVLLVLFVSVLAH 518
DB 481 ILFVFAEAGVGVNVDRESEDEVRTMLGHTPGEMFMTCSYISPVLLVLFVSVLAH 540
OY 519 EEMLGGEITYPSWSTIYGVWMTGTVVSCIPLYITIKLLITPGNCINRIKTIQORE 573
DB 541 KPLTYDDYIFPPMANWGMGIALSSMVLPTVITYIKFLSTOGSLMERLAVGITPE 595
```

RESULT 9
US-08-240-783B-3
Sequence 3, Application US/08240783B
Patent No. 5756348
GENERAL INFORMATION:

```

APPLICANT: Smith, Kelli
APPLICANT: Borden, Laurence A.
APPLICANT: Branche, Theresa
APPLICANT: Hartig, Paul R.
APPLICANT: Weinstanek, Richard L.
TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,783B
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39875-A-PCR-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HUMAN NORADRENALINE TRANSPORTER
US-08-240-783B-3

Query Match          51.1%; Score 1605.5; DB 1; Length 617;
Best Local Similarity 51.6%; Pred No. 14e-138;
Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;

1 MPPSDAPP---APTAPPDPLPA-TTAQ-----KSRVSVVSLT-----PARQRETMAKAEF 47
6 MNPQVQPEHNGADTGPDEQLARKTAELLVYKERNGVQCLAPRQDDAQPRETWCKKIDF 65
48 LLAVVGFAVDLGNVWRFPYICQNGGGAFLIPYCWMLFEGGLPFLLELALCOYHRCGL 107
66 LLSVVGFAVDLGNVWRFPYICQNGGGAFLIPYTLFLIAGMPLFYMETALCOYNREGAA 125
108 TLMKRICPALKGVGAICMIDIDYMGVYNTIIGMAVYVLIASINSVLPTSCDNEAN 167
126 TWK-ICPEFKVGVAVIILALYGVFYVITAMSLYIFSSF-TLN--LPMTDCGHTWN 181
168 TPLCT-----PVTSPTQ--NPNSSTPAKEFEERNVLEDOHKSNGLDMDGPTKPSLALCV 218
182 SPNCIDPKLLNGSVLGNHTKYSKYFTPAAEFYERGVHLHSSSGHDIGLPQWOLLTCL 241
219 FGVFVLYVFSLMKGYRSAGKYVWVATALAPYVVLILLANGVLLPGATBSIRIYLLPEWKK 278
242 MVVYVLYVFSLMKGYRSAGKYVWVATALAPYVVLILLANGVLLPGATBSIRIYLLPEWKK 301
279 LONSXVWIDAASQIFESLCPGFTLLALSSYNNKFNNCYRDALLTSINCLTSLAGFYI 338
302 LKEATVWIDAATQIFESLCPGFTLLALSSYNNKFNNCYRDALLTSINCLTSLAGFYI 361
339 FSVLGYMAHVONKSIIEVGLGPGVLFVYVPAIATMTGVSVAIIFLMLITLGLDSTP 398

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Db          362 FSLIGYMAHEHKNVEDVATEGAGLVEFLYPEAISTLSGSTFWAVVFWMLALGDSMM 421
QY          399 GGEUENTTALCOEYPRVLRHREVFYAVLLLEIYICALPTTYGCVYVLDLVNIGPGIA 458
Db          422 GGEAVITGLADDF-OVLKRHRKLFFEGVTFSTFLALCITKGGIYVLTLDTPAAGTS 480
QY          459 ILFVFAEAGYGVWVDRFSEDVYRTMLGHTPGMFWRCWMSYISVFLVLFVSVLAH 518
Db          481 ILFVMEAGYGVWVDRFSEDVYRTMLGHTPGMFWRCWMSYISVFLVLFVSVLAH 540
QY          519 EEMLGEYTYPSMSTIVGWMTGTVCIPLYIYKLLITPGNCINRIKTQRP 573
Db          541 KPLTYDDYIFPPWAMVWGICALSSMVLVPIYVYFLSTQSLMERLAYGITPE 595

RESULT 10
US-08-753-985-11
Sequence 11, Application US/08753985
Patent No. 5759788
GENERAL INFORMATION:
APPLICANT: Fremeanu Jr., Robert T.
APPLICANT: Caron, Marc G.
APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,985
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879617
FILING DATE: 01-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6558
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Brain -norepinephrine transporter
FEATURE:
NAME/KEY: Active-site
LOCATION: 95..96
OTHER INFORMATION: /note="Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note="Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note="Leucine zipper motif"

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NAME/KEY: Active-site
LOCATION: 109..110
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 116..117
OTHER INFORMATION: /note= "Leucine zipper motif"
US-08-753-985-11

Query Match
Best Local Similarity 51.1%; Score 1605.5; DB 1; Length 617;
Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;

QY 1 MPPSDAPP---APTAPPPDLPA-TTAQ-----KSRSVVSLT-----PARORETAKKAEF 47
DB 6 MNPQVQPNNGADTPEQPLRARKTAELLVYKERNVOCLAPRQDQAPRETWKKIDF 65
QY 48 LLAVGFADLGNVRRFPYICQNGGAFLLPYCYMLFGLPLFLELALGOYHRCGL 107
DB 66 LLSVGFADLGNVRRFPYICQNGGAFLLPYCYMLFGLPLFLELALGOYHRCGL 125
QY 108 TLMKRICALKGVGAICMIDYMGMYNTIIGMAYVYLIALASINSVLPSTGDNEMN 167
DB 126 TWMK-ICPEFGKGVAVLIALYVGFYNNVIAVSLYLFSSF-TLN--LPMTDGHWN 181
QY 168 TPLCT-----PVTSPT--NPNSSTPAKEFEERNVLEOHKSNGLDMDGPIKPSALCV 218
DB 182 SPNCIDPKLNGSVLGNHTKYSKYFTPAEYERGVHLHSSGIDHIGLPQMLLCL 241
QY 219 FGVFVLVFSLMKGVRSAGKVVWTALAPYVLLILLAGVTLPGATEGIRYLTPEMHK 278
DB 242 MVVYVIVLFSLMKGVRSAGKVVWTALAPYVLLILLAGVTLPGATEGIRYLTPEMHK 301
QY 279 LQNSKVMIDASQIFFSIGPFGTLLASVYKFNKNCYRDALITSSINCLTSLAGVI 338
DB 302 LKEATVWIDATQIFFSIGAGGVILAFASYNKFNKNCYRDALITSSINCLTSLAGVI 361
QY 339 FSVLGMAYHONKSIEEVLGEGPGLVFIYVPAIATMGSVFMAIIFLMLITGLDSTF 398
DB 362 FSLIGYMAHEKVNIEDVATEGAGLVFLIYPAISTLSGTFMAVVFVMLALGLDSM 421
QY 399 GGLVAVTALCDEYRVLGRHREVFVAVLLFIYICALPTTYGGVYLVLDLNVYGPGLA 458
DB 422 GGMVAVITGLADD-QLKRRHKLTFPGVTFSTFLALFCITKGGIYVTLTLDTPAAGTS 480
QY 459 ILFVFAEAGYCWYGVDRSEEDVRYTMIGHTPGMFMTQMSYISPVLLVLFVSVLAH 518
DB 481 ILFAVLAEMAGVSWFYGVDRSNDIQOMGFRPGLYWRKCKWFPAPLLEFVVVSIINF 540
QY 519 EEMLGGEYTPSMSTIVGWMVTGTVSCIPLYIYKLLITPGNCINRIKTQRP 573
DB 541 KPLTYDDIYFPWMWVGIALSSMVLPIYIVIKFLSTOGSLMERLAYGITPE 595

RESULT 11
US-09-084-813-3
Sequence 3, Application US/09084813
Patent No. 6127131
GENERAL INFORMATION:
APPLICANT: Smith, Kelli
APPLICANT: Borden, Laurence A.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084, 813
FILING DATE: 26-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39875-AZ-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: HUMAN NORADRENALINE TRANSPORTER
US-09-084-813-3

Query Match
Best Local Similarity 51.1%; Score 1605.5; DB 3; Length 617;
Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;

QY 1 MPPSDAPP---APTAPPPDLPA-TTAQ-----KSRSVVSLT-----PARORETAKKAEF 47
DB 6 MNPQVQPNNGADTPEQPLRARKTAELLVYKERNVOCLAPRQDQAPRETWKKIDF 65
QY 48 LLAVGFADLGNVRRFPYICQNGGAFLLPYCYMLFGLPLFLELALGOYHRCGL 107
DB 66 LLSVGFADLGNVRRFPYICQNGGAFLLPYCYMLFGLPLFLELALGOYHRCGL 125
QY 108 TLMKRICALKGVGAICMIDYMGMYNTIIGMAYVYLIALASINSVLPSTGDNEMN 167
DB 126 TWMK-ICPEFGKGVAVLIALYVGFYNNVIAVSLYLFSSF-TLN--LPMTDGHWN 181
QY 168 TPLCT-----PVTSPT--NPNSSTPAKEFEERNVLEOHKSNGLDMDGPIKPSALCV 218
DB 182 SPNCIDPKLNGSVLGNHTKYSKYFTPAEYERGVHLHSSGIDHIGLPQMLLCL 241
QY 219 FGVFVLVFSLMKGVRSAGKVVWTALAPYVLLILLAGVTLPGATEGIRYLTPEMHK 278
DB 242 MVVYVIVLFSLMKGVRSAGKVVWTALAPYVLLILLAGVTLPGATEGIRYLTPEMHK 301
QY 279 LQNSKVMIDASQIFFSIGPFGTLLASVYKFNKNCYRDALITSSINCLTSLAGVI 338
DB 302 LKEATVWIDATQIFFSIGAGGVILAFASYNKFNKNCYRDALITSSINCLTSLAGVI 361
QY 339 FSVLGMAYHONKSIEEVLGEGPGLVFIYVPAIATMGSVFMAIIFLMLITGLDSTF 398
DB 362 FSLIGYMAHEKVNIEDVATEGAGLVFLIYPAISTLSGTFMAVVFVMLALGLDSM 421
QY 399 GGLVAVTALCDEYRVLGRHREVFVAVLLFIYICALPTTYGGVYLVLDLNVYGPGLA 458
DB 422 GGMVAVITGLADD-QLKRRHKLTFPGVTFSTFLALFCITKGGIYVTLTLDTPAAGTS 480
QY 459 ILFVFAEAGYCWYGVDRSEEDVRYTMIGHTPGMFMTQMSYISPVLLVLFVSVLAH 518
DB 481 ILFAVLAEMAGVSWFYGVDRSNDIQOMGFRPGLYWRKCKWFPAPLLEFVVVSIINF 540
QY 519 EEMLGGEYTPSMSTIVGWMVTGTVSCIPLYIYKLLITPGNCINRIKTQRP 573
DB 541 KPLTYDDIYFPWMWVGIALSSMVLPIYIVIKFLSTOGSLMERLAYGITPE 595

Search completed: July 18, 2003, 22:02:01
Job time : 26 secs

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,722A
FILING DATE: 07-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1173-406P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 619 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..619
OTHER INFORMATION: /note= "Dat1 sequence, see Fig. 5"
US-08-301-722A-4

Query Match      48.68; Score 1525; DB 1; Length 619;
Best Local Similarity 49.24; Pred. No. 3.2e-131;
Matches 279; Conservative 105; Mismatches 157; Indels 26; Gaps 5;

QY 14 PPDLPATTAGKSRVSVVSLTPARORETWAKKAEFLAVGFAVDLGVMRFPYICYONGG 73
DB 50 PPGTP-----VEAQRERWTKKIDFLSVIGFAVDLAWMRFPLCYKNGG 95
QY 74 GAFLIPYCVMLLEGLPLFLELALGQYHRCGLTLMKRITCPALKGVAICMIDIYGM 133
DB 96 GARLVPLFLFMVLAGPLFYMELALGQFNAGAGVWK-ICPYLKGVFVLLISFYGF 154
QY 134 YVNTIIGNAVYIILASIASINSVLPMTSCNEMNTPLCTPVTSPQINPN-----SSTP 186
DB 155 FYNVIIAMALHYF--FSSEFTMDLPWICHNTNNSPNCSDAHASNSDGLGNDTGTTP 211
QY 187 AKFEFFERNVLEOKSNGLDMDGPIKPSIALCVFQVFLVYFSLMKGVRSAGKYVWYATA 246
DB 212 AAEYFERGVHLHOSKIDDLGPPRWQLTACLVLVLYLFLSLMKGVKISGKYVWYATM 271
QY 247 PYVVLILLAGVTLPGATEGIRYVYLPWEHKLQNSKRWIDAASQIFSLGPGFTLLAL 306
DB 272 PYVVLALLRGVTLPGAMDGIKAYLSVDEYRICEASVWIDAMQVCFSLGCVGLIAF 331
QY 307 SSYNKFNNNKCYRALITSSINCLTSPFLAGVIVSVLCYMAHVONKSIEEVLGPGCLVFI 366
DB 332 SSYNKFTNNKCYRALITTSINSLSLTSFSSGFFVSEFLGYMAQKHNPTRDVAIDGPGCLIFI 391
QY 367 VYPEAIAATMGVFWATIFFLMLITLGLDSTFGLEAVTALCDEYPRVGRHREPVAV 426
DB 392 IYPEAIAATLPLSSAMAFAVFLMLITLGLIDSAMGMSVITGLVDF-QLLHRHRELFTLG 450
QY 427 LLLFLIYICALPTTYGGVYLVLDLNNYGPGLAILFVFAEAGVCWVYGVDRFSEDEVYM 486
DB 451 IYLAFTLLSLFCVTNGIYVFTLLDHAAGTSLIFGLIAIGVAMFYGVQGFSDDIK 510
QY 487 LGHTPGHFMATCSYISPVFLVLVLFVSVAHEMELGGETYTPSWSTTVGVWMTGTTVSC 546
DB 511 TGORPMLYWRLYKLVKLVSPCLLYVVVVSIVTFRRPHYGAYIFPDWANAIGMIATSSAM 570
QY 547 IPLYIYKLLITPGNCINRIKTIORPE 573
DB 571 VPYIATYKFCSLPGSPREKLAIVATPE 597
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